

## Structure of HTPL and alignment of Patched motifs.

**FIG. 1A**

HTPL-L (954 a.a.)



HTPL-S (767 a.a.)



**FIG. 1B**

Patched motif

	10	20	30	40	50	60	70	80
consensus	*	*	*	*	*	*	*	*
HTPL-L	1 VISSKIRYTFTPDDIRSYTERGSRSEHEPL-VERKFFPGDGYPIRSFSLLITAKARNS-NILDITYLNEVVQVYNDIFISTNV	78						
gi	1825729	162 deedleehyTPVGSPAKAERRFVQGHFTmDSYRFSASRRSTEANFVSLLVSVYSD-SLLDPATFAEVSKLDGAVQDLR	240					
gi	1707052	47 NPLSDAVYLFTPLGAQSKMERMISHEKWPL-TDNNYIPGRAVTQSREIQVTALARNSNILDPKFANAVYQLDKYIQTTRV	125					
gi	3892144	22 NVVYSLLMIFGPy---SYTERRIHDAWPL-VDGTFVAGRAVTQSREVQAVAVARSQGNILDRCVFSNELKLMEASFIRNNI	97					
		49 LRVDDPSYVFPTPSDARWRREISVFENWNWL-DENKFPLGKSFEARKFVNILIRAKDGGSIIMRDNVNLHEIILNQWIMNNI	127					
consensus	*	*	*	*	*	*	*	*
HTPL-L	79 TIPVSG--ITLSFKDLCMRFCDINCPVNQHYNGQILRSNLHNSRIDLTPTMTFFGTRKIVLGPNFGGVKLDBN---PGN-	152						
gi	1825729	241 VAREKG--SQIOYOQQVCARYRALCVPNPILLYAWQVNKTLNLS--SISFPAYNEGRHPLYLTTGFFGGYILGGS--LGmg	313					
gi	1707052	126 RVLHNG--HYYSYKNLCLQYKNGGCPSNKHT---HILSDLHNHGENTYPRFGSEGGYIGSSLGGVTVMKGenetDI-	199					
gi	3892144	98 TVQFSN--RTWSFADLCLAGpDGRCANNDHII---QLASRLHQHGGINITYPTVRLSDKSAYTASALGVKLAKgdngeNI-	171					
		128 SIPTDD1kFNLTyQDLCLSY-DWVCGANEHIQ-MLLRNDVNQIILDLHFRGGTKDTPVYLGIFGDQFFFQn---GT-	200					

## FIG. 1B

### Patched motif (Continued)

<p>170      180      190      200      210      220      230      240</p> <p>* . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .  </p> <p>consensus 153 --IKSVKAIVLYYRLKRDPEEEVEEDSKEWELSLEFDYLENEYASD-HIQ-VT1FSDQVLED--ELVRNGLLTLPFFVGFA 226</p> <p>HTPL-L 314 QILLRAKAMRLLYLYLKTEDPEYDVQSKQWLTHILLDQFTNIKNIL-ALKKIEVVHFTSLRQLEFEATSVTVIPVFHLAYI 392</p> <p>gi 1825729 200 --LASAKAWFMITYHLKFPEEMSYSISGEWELELGRMLTOYPEDP-YIS-ITYFHSQLTLAD--ELKRNADTLIPRFILISIT 273</p> <p>gi 1707052 172 --IVEATAWLLIYQLKFYPNEISYVSGLWEREFKNCMDYKKQAKYIS-ITYFHSQLTLSD--ELNRNAERLAPKFIGAFV 246</p> <p>gi 3892144 201 --LSDAKLTQLFYFLKQDKMVEEYSSKFSYALETFLNQVYSSD-VIT-LSFAHYQSLED--GLDENAKAFVPNFVUVSSF 274</p> <p>250      260      270      280      290      300      310      320</p> <p>* . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .  </p> <p>consensus 227 ILVTFSILTSVLRLAS-GSLHDIDWVRSKPIAILLGVLTPLMAIVSAFGLLFWLGFRENSIVCVMMPFLVL- 293</p> <p>HTPL-L 393 LILIAVTSCFRF-----DCIRNRMCMVAAGFVISAFLAIVSGFGLLLHIGVPFVIIIVANSPEFLIL- 452</p> <p>gi 1825729 274 LLIVFSTLCSLSFID-GSFSDIDWVLSPKILSILGVVSSAGIAILTGVGFLSLMGMPFLVL----- 340</p> <p>gi 1707052 247 ILVCFSVLCISIVTIK-GGGYIDWVTKPILSVLGVSNAGMGLIASAMGMLTYLEIYQNDIIIAVAMPFLV----- 313</p> <p>gi 3892144 275 VLAMYALVSSFTLKSATKIDWISSKPWLAAAGMFSTVLSIISAFGFLFILGVRYNVINTIIPFLIigefqsfkmekn 354</p> <p>330      340      350      360      370      380      390      400</p> <p>* . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .  </p> <p>consensus 294 --AIGVDDDMFLMVHAWRRTTRSLSYVKKRMGEVYLEEAGPSITITSNLNSFGIGAITTPTEIQLFCIYTAVAIFEDFLY 370</p> <p>HTPL-L 453 --GGVDDDMFLIMISAWHKTNLAGDIRERMSNYSSKAAVSITITITNLLALYTGIMSSFRSVQCFCIYTGTLLFCYFY 529</p> <p>gi 1825729 341 --AVGVDNMFLMVAAVRTSRTHYHERMGECLADAavisllitsstdvlsfgvgaitttipaivoqfcvtytgvalffafy 417</p> <p>gi 1707052 314 --AVGTDNMFLMVASLKRIDRNLYKDRIACMADAASILITALTDALSFGVGTITTIIPAQIFCIYTMCALLTFAV 390</p> <p>gi 3892144 355 qipaIGDDMFLMNACWDQTSTSLSUPERMSKTLSHAGVAVTITNVTDMSFAIGCITDLPGIQFFCIRYACVSVAFSYFY 434</p> <p>410      420      430      440      450      460      470      480</p> <p>* . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .   . . . * . . .  </p> <p>consensus 371 QLTFFAAIMAIAQKYEMKGRHSLSFLRR----AVDAAETESP-----QRLDSRGSAK----- 416</p> <p>HTPL-L 530 NITCFGAFMALDGKRE---VVCLCW----LKADPKWPS-----FRKFCCCFPFG----- 571</p> <p>gi 1825729 418 QITFFAAACLAAMKHEASGRNLSFLIE---AVSAEKKTSLSIst--FQRLENLGSVPd----- 468</p> <p>gi 1707052 391 QLTFFCAILVYTRIEEQGLHSIWLrp---AVTYSSTSPLn---VKLFWLGSQPckplpscgtvss----- 450</p> <p>gi 3892144 435 QLTFFSGAMAIMGEVEREKRHCLFFYrtfqLVDISKMNEEadsklQQIKRSASApfnlysssssssssssssskkt 514</p>	<p>2/18</p> <p>FIG. 1</p>
---	---------------------------

**FIG. 1B**  
**Patched motif (Continued)**

consensus	417	490	500	510	520	530	540	550	560
HTPL-L	572	-----	SSKSHE--AEQ-	AVVKFFFLNIYCPFLINPKVRVCFULLVIVLIAIYGCINMKEGLDDPAKL	475				
gi_1825729	469	-----	SVPDEHgtdIH--	PMSLFFFDRDYFGPFLTRSESKYFVVFIYVLYIISIYGCFCFHVQEGLDLRNL	632				
gi_1707052	451	-----	tssvstmtsqtSPASKH--	AATSFFRNWYAPVLMHPVVRGIAVWFVYLLGASYGCSRRIEGLEPVNL	528				
gi_3892144	515	ipaefawkeqqspnss1	SSKSKSD--REEKdRIVHFIGK1YGPFFILNSVRIFSGLIFVYVTLAIAMYGCYNFREGLNPGNLL	592					
consensus	476	570	580	590	600	610	620	630	640
HTPL-L	633	ASDDSYTTPYFNVEENYFS	DYGRPMVIVTKKVDWDRQKLLNC	TKFPEKNVY-VDKNLTEFWLDAYVQLK-GNS	555				
gi_1825729	529	LVEDSYAIPHYRLLekYFWKYGQQQ	QIVINNAPDLRNHTSRDRHAMVLDEATSKAIGM	GMEVSQFWLFEMER-YYQKELE	709				
gi_1707052	523	LVDSSYATPHYRVLekHYGASLQIVVSNPPD	DLRDPVERINMDKMASTFANCKVAIGDDSVQFWLREMQ--VSEEIHK	607					
gi_3892144	593	VTN	DHYIAKYFSDI-KHFWRIGAQQLHVAVLNPNNTISENRNELLKVVA	SAFENTQYTGLGREGTVFELLEYLNLSLNAE	600				
consensus	556	LEDEEEFWFYDLDLEWFL-KSPGFSHWVGDLJWDN-KTDYETTIVKKFRFTTGGDLS	TRRLLKTWGRVADEYPDFN	671					
HTPL-L	710	QDPNEKNTFMNNIPD	ELNSFPNFQH-----DI-NISSSNELISSRGF-IQTTDVSSAKKKILLFQLRRIA-EDCQIP	633					
gi_1825729	608	VQIID-SSFYGLHHFL-ASKTNPLAEDIYWGPM	PDDDNGMTMVKSFREILLGMKDLVTTMDQTDATMSFREVAARWPEFNV	779					
gi_1707052	601	IQYDN-EKFYDHAAQYI-YSDMSQPWVVDVWIG--RNNNNSERLI	KTFRFMIGMRDISTS	TTKQTEATNTFREIASRFEQYN	685				
gi_3892144	672	VEDTERLWTKLNSWLK-YTGGSTQWASNLIKIN-----	KTDGSFQAFRQIALKNFVEBNDHKHAQQLRDIADHQ	P-FN	676				
consensus	634	730	740	750	760	770	780	790	800
HTPL-L	780	LMVYNQA-	-----AFFLDQILSIGPTTIQSIIWTLICMAVVCFLFIPNPNTVVFITVSI	686					
gi_1825729	686	VTTEMP1-----	FIYFDQYAILEDTVRNVLVASAMFIVSLLIIPYPLCLSLWVTFAI	832					
gi_1707052	677	VTTYMPL-----	WMFTDQYALVVPNTMQDLIVAVACMLVISALLIPQPVCSFWVAVTI	738					
gi_3892144	745	VVYHEVsfgnrkilndfisshscyaqknipkla	FADQYLILPATIQNVISLLCMAVVSFLVPSLPGFVIFVSI	729					

**FIG. 1B**  
Patched motif (continued)

	810	820	830	840	850	860	870	880
consensus	.....*	.....*	.....*	.....*	.....*	.....*	.....*	.....
HTPL-L	687 ASIDIGVFGFLSLWGVLDLDPISMITIIMSIGFSVDFSAHIAHYFYRSHGSETPDERLADALEALGWPVIAALSTILCVL	766						
gi 1825729	833 GSVIVGVTGEMAFWKVNLDLSIMINIVCTGFSFDSAHISYAFV-SSSQPSVNOKSVEALYLIGYPVLOSAISTIIGVC	911						
gi 1707052	739 ASIDFGVIGYMTLWGVNLDAISMITHIMSIGFSVDFSAHIAHYGYVVSRED-TAAGRVEAKSALSALGWPLSQGAMSTILAVS	817						
gi 3892144	730 GSIDLGVLGFMNTLWNVNLDAAISMITHIMSIGFSVDFSAHITYAYVISKES-TTSARVCDALGDLGWPAQGAMSTILAVS	808						
	825 VSINIGVFGYMTLWGVNLDAVSMISIIMSIGFAVDLSAHIITYAFTVSHG--DTKQRVIGALETLGWPPIFGQGASSTIAGIS	902						
	890	900	910	920	930	940		
consensus	.....*	.....*	.....*	.....*	.....*	.....*	.....*	
HTPL-L	767 PLLFVPSYMVVFEEKTIFLVVVIGLLHGLLFLPIILSFLFTV-----IRTSNAKIKKPSSI	821						
gi 1825729	912 VLAIAAKAYIFRFFFKIMFLUMIFGAHGLIFIPVFLFFGRFI-----	954						
gi 1707052	818 VLADIPAYMIVTFFFKVVLISISGLLHGGLVFLPVLLSIFVRgcciipssphGHPSAQKIEKOIRI	882						
gi 3892144	903 ILYTVDAYILLVFEEKTIVLMLIGAITHGLFFIPIFLSLFPV-----EFFRIPKSSEL	954						

## Structure of the HTPL gene (Chr. 10p12.1)

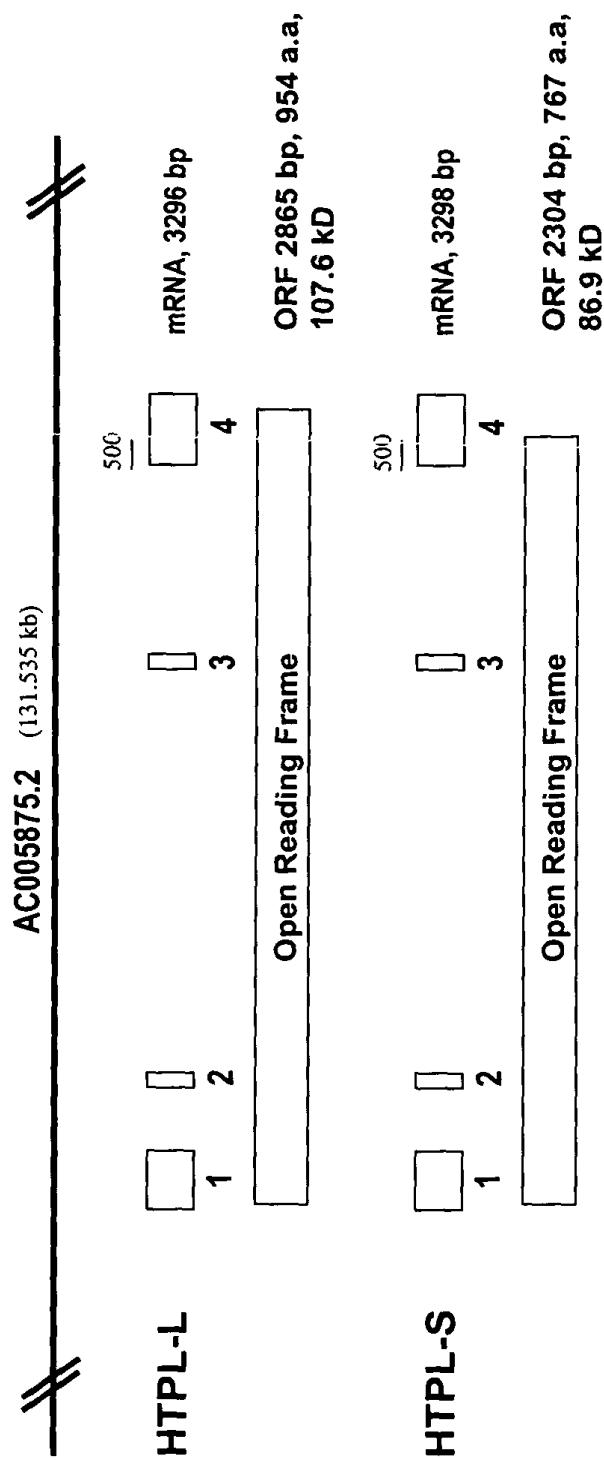


FIG. 2

**HTPL-L**

**nt: SEQ ID NO: 1**  
**aa: SEQ ID NO: 3**

CAGGAAACCGTCTGGTGGGATCTCCGCAGCTGCTTTCACCTGCTGTTCCCTC	52
M P W V E P	6
CTGCGCTTCCTAACAGAGGAAGAACATCA ATG CCG TGG GTG GAG CCC	95
K P R P G P E Q K P K L T	19
AAG CCC AGG CCG GGG CCG GAG CAG AAG CCC AAG CTC ACC	134
K P D S A T G P Q W Y Q E	32
AAA CCG GAC TCT GCC ACC GGG CCG CAG TGG TAC CAG GAA	173
S Q E S E S E G K Q P P P	45
TCT CAG GAA TCG GAG TCG GAA GGC AAG CAG CCA CCC CCG	212
G P L A P P K S P E P S G	58
GGA CCC CTG GCA CCC CCG AAA TCC CCC GAA CCC TCA GGA	251
P L A S E Q D A P L P E G	71
CCC CTG GCG TCG GAG CAG GAT GCA CCC CTG CCA GAG GGG	290
D D A P P R P S M L D D A	84
GAC GAT GCA CCC CCC CGG CCG TCG ATG CTG GAC GAT GCA	329
P R L P L E L D D A P L P	97
CCC CGC CTG CCG CTG GAG CTG GAC GAT GCA CCC CTG CCG	368
E E E T P E P T A I C R H	110
GAG GAG GAA ACC CCC GAA CCC ACG GCC ATC TGC AGG CAC	407
R H R C H T D C L E G L L	123
CGG CAC CGC TGT CAC ACC GAC TGC CTA GAG GGG CTG CTG	446

**FIG. 3**

S	R	T	F	Q	W	L	G	W	Q	V	G	A	136
TCC	CGC	ACC	TTC	CAG	TGG	CTG	GGG	TGG	CAG	GTG	GGC	GCG	485
H	P	W	I	F	L	L	A	P	L	M	L	T	149
CAC	CCC	TGG	ATC	TTC	CTG	CTG	GCG	CCC	TTG	ATG	CTG	ACA	524
A	A	L	G	T	G	F	L	Y	L	P	K	D	162
GCC	GCG	CTG	GGC	ACC	GGC	TTC	CTG	TAC	CTA	CCC	AAG	GAC	563
E	E	E	D	L	E	E	H	Y	T	P	V	G	175
GAA	GAG	GAA	GAC	CTA	GAG	GAG	CAT	TAC	ACC	CCT	GTG	GGG	602
S	P	A	K	A	E	R	R	F	V	Q	G	H	188
AGC	CCG	GCC	AAG	GCG	GAG	CGG	CGC	TTC	GTC	CAG	GGC	CAT	641
F	T	T	N	D	S	Y	R	F	S	A	S	R	201
TTC	ACC	ACC	AAC	GAC	TCC	TAC	CGC	TTC	TCC	GCC	TCC	AGG	680
R	S	T	E	A	N	F	V	S	L	L	V	V	214
AGG	AGC	ACC	GAA	GCC	AAT	TTC	GTC	TCG	CTT	CTG	GTG	GTC	719
S	Y	S	D	S	L	L	D	P	A	T	F	A	227
TCC	TAC	AGC	GAC	TCA	CTG	CTG	GAC	CCA	GCT	ACC	TTT	GCA	758
E	V	S	K	L	D	G	A	V	Q	D	L	R	240
GAA	GTC	AGC	AAA	CTG	GAC	GGC	GCG	GTG	CAG	GAT	CTG	CGC	797
V	A	R	E	K	G	S	Q	I	Q	Y	Q	Q	253
GTG	GCG	CGG	GAA	AAG	GGA	AGC	CAG	ATC	CAG	TAC	CAG	CAG	836
V	C	A	R	Y	R	A	L	C	V	P	P	N	266
GTG	TGC	GCG	AGG	TAC	AGG	GCG	CTC	TGC	GTG	CCC	CCC	AAC	875
P	I	L	Y	A	W	Q	V	N	K	T	L	N	279
CCG	ATC	CTG	TAC	GCC	TGG	CAG	GTG	AAC	AAA	ACG	CTC	AAC	914
L	S	S	I	S	F	P	A	Y	N	H	G	R	292
CTG	AGC	AGC	ATC	TCC	TTC	CCC	GCC	TAC	AAC	CAC	GGC	AGG	953
H	P	L	Y	L	T	G	F	F	G	G	Y	I	305
CAT	CCC	CTC	TAC	CTG	ACC	GGC	TTC	TTC	GGA	GGA	TAC	ATC	992

FIG. 3

L	G	G	S	L	G	M	G	Q	L	L	L	R	318
TTG	GGG	GGC	AGC	CTA	GGA	ATG	GGC	CAG	TTA	CTC	CTG	CGG	1031
A	K	A	M	R	L	L	Y	Y	L	K	T	E	331
GCC	AAA	GCC	ATG	CGG	CTG	CTG	TAC	TAC	CTG	AAG	ACC	GAG	1070
D	P	E	Y	D	V	Q	S	K	Q	W	L	T	344
GAC	CCT	GAG	TAC	GAC	GTG	CAG	AGC	AAG	CAG	TGG	CTC	ACC	1109
H	L	L	D	Q	F	T	N	I	K	N	I	L	357
CAT	TTG	CTC	GAT	CAA	TTT	ACC	AAC	ATT	AAG	AAC	ATC	TTG	1148
A	L	K	K	I	E	V	V	H	F	T	S	L	370
GCC	TTG	AAA	AAA	ATT	GAG	GTA	GTC	CAC	TTT	ACA	TCG	CTT	1187
S	R	Q	L	E	F	E	A	T	S	V	T	V	383
TCC	AGA	CAA	CTG	GAA	TTT	GAG	GCA	ACT	TCT	GTG	ACT	GTG	1226
I	P	V	F	H	L	A	Y	I	L	I	I	L	396
ATC	CCT	GTG	TTT	CAC	CTG	GCA	TAC	ATT	CTC	ATC	ATT	CTG	1265
F	A	V	T	S	C	F	R	F	D	C	I	R	409
TTT	GCA	GTC	ACA	TCA	TGC	TTT	AGG	TTT	GAC	TGC	ATA	CGA	1304
N	K	M	C	V	A	A	F	G	V	I	S	A	422
AAC	AAA	ATG	TGT	GTT	GCG	GCC	TTT	GGA	GTG	ATT	TCT	GCT	1343
F	L	A	V	V	S	G	F	G	L	L	L	H	435
TTC	TTG	GCA	GTG	GTG	AGC	GGC	TTT	GGC	CTG	CTG	TTG	CAC	1382
I	G	V	P	F	V	I	I	V	A	N	S	P	448
ATT	GGG	GTG	CCA	TTT	GTC	ATC	ATA	GTG	GCC	AAT	TCA	CCA	1421
F	L	I	L	G	V	G	V	D	D	M	F	I	461
TTT	CTT	ATT	CTA	GGT	GTT	GGG	GTC	GAT	GAC	ATG	TTT	ATC	1460
M	I	S	A	W	H	K	T	N	L	A	G	D	474
ATG	ATT	TCT	GCC	TGG	CAT	AAG	ACC	AAC	CTT	GCA	GGT	GAC	1499
I	R	E	R	M	S	N	V	Y	S	K	A	A	487
ATA	CGA	GAG	CGG	ATG	TCC	AAT	GTC	TAT	TCA	AAA	GCG	GCA	1538

FIG. 3

V	S	I	T	I	T	T	I	T	N	I	L	A		500
GTG	TCT	ATT	ACA	ATC	ACC	ACC	ATC	ACT	AAC	ATC	CTG	GCC		1577
L	Y	T	G	I	M	S	S	F	R	S	V	Q		513
TTA	TAT	ACA	GGG	ATT	ATG	AGC	TCT	TTT	AGG	TCC	GTA	CAA		1616
C	F	C	I	Y	T	G	T	T	L	L	F	C		526
TGT	TTT	TGC	ATC	TAT	ACA	GGA	ACG	ACC	CTG	TTA	TTT	TGC		1655
Y	F	Y	N	I	T	C	F	G	A	F	M	A		539
TAT	TTT	TAT	AAC	ATC	ACG	TGT	TTT	GGA	GCA	TTT	ATG	GCC		1694
L	D	G	K	R	E	V	V	C	L	C	W	L		552
TTG	GAT	GGT	AAA	AGA	GAA	GTA	GTC	TGC	CTA	TGC	TGG	TTG		1733
K	K	A	D	P	K	W	P	S	F	K	K	F		565
AAA	AAG	GCT	GAC	CCA	AAA	TGG	CCC	TCA	TTT	AAA	AAG	TTC		1772
C	C	F	P	F	G	S	V	P	D	E	H	G		578
TGC	TGT	TTC	CCA	TTT	GGT	TCT	GTC	CCA	GAT	GAA	CAT	GGA		1811
T	D	I	H	P	M	S	L	F	F	R	D	Y		591
ACT	GAT	ATC	CAT	CCA	ATG	AGT	TTG	TTT	TTT	AGA	GAC	TAT		1850
F	G	P	F	L	T	R	S	E	S	K	Y	F		604
TTT	GGC	CCC	TTT	CTC	ACA	AGG	AGT	GAG	TCC	AAG	TAT	TTT		1889
V	V	F	I	Y	V	L	Y	I	I	S	S	I		617
GTA	GTC	TTT	ATA	TAT	GTT	TTG	TAC	ATC	ATA	AGC	AGT	ATA		1928
Y	G	C	F	H	V	Q	E	G	L	D	L	R		630
TAT	GGG	TGT	TTC	CAT	GTG	CAG	GAA	GGT	TTA	GAC	CTT	CGA		1967
N	L	A	S	D	D	S	Y	I	T	P	Y	F		643
AAT	CTG	GCA	AGT	GAC	GAT	TCC	TAC	ATC	ACA	CCA	TAT	TTT		2006
N	V	E	E	N	Y	F	S	D	Y	G	P	R		656
AAC	GTA	GAG	GAG	AAT	TAT	TTT	TCA	GAT	TAT	GGT	CCC	AGG		2045
V	M	V	I	V	T	K	K	V	D	Y	W	D		669
GTT	ATG	GTT	ATT	GTT	ACT	AAA	AAA	GTT	GAC	TAC	TGG	GAT		2084

FIG. 3

10/18

K	D	V	R	Q	K	L	E	N	C	T	K	I	682
AAA	GAT	GTT	AGG	CAA	AAA	CTG	GAA	AAC	TGT	ACT	AAA	ATT	2123
F	E	K	N	V	Y	V	D	K	N	L	T	E	695
TTT	GAA	AAA	AAT	GTC	TAT	GTA	GAT	AAA	AAT	CTT	ACA	GAG	2162
F	W	L	D	A	Y	V	Q	Y	L	K	G	N	708
TTT	TGG	TTA	GAT	GCA	TAT	GTG	CAA	TAT	TTA	AAA	GGT	AAC	2201
S	Q	D	P	N	E	K	N	T	F	M	N	N	721
AGC	CAA	GAT	CCT	AAT	GAG	AAG	AAT	ACT	TTT	ATG	AAC	AAT	2240
I	P	D	F	L	S	N	F	P	N	F	Q	H	734
ATT	CCT	GAT	TTT	TTA	AGC	AAT	TTT	CCA	AAT	TTT	CAG	CAT	2279
D	I	N	I	S	S	S	N	E	I	I	S	S	747
GAT	ATT	AAT	ATT	TCT	TCA	TCA	AAT	GAA	ATC	ATT	TCT	TCC	2318
R	G	F	I	Q	T	T	D	V	S	S	S	A	760
CGG	GGC	TTC	ATT	CAG	ACA	ACA	GAT	GTT	TCT	TCC	TCA	GCC	2357
K	K	K	I	L	L	F	Q	L	R	R	I	A	773
AAA	AAG	AAA	ATA	TTG	TTA	TTC	CAA	TTA	CGA	CGC	ATA	GCT	2396
E	D	C	Q	I	P	L	M	V	Y	N	Q	A	786
GAA	GAC	TGT	CAA	ATT	CCC	CTA	ATG	GTG	TAT	AAC	CAG	GCA	2435
F	I	Y	F	D	Q	Y	A	A	I	L	E	D	799
TTT	ATA	TAT	TTT	GAT	CAG	TAT	GCT	GCA	ATA	TTA	GAA	GAC	2474
T	V	R	N	V	L	V	A	S	A	A	M	F	812
ACT	GTT	AGA	AAT	GTA	TTG	GTT	GCA	TCA	GCA	GCT	ATG	TTC	2513
I	V	S	L	L	I	P	Y	P	L	C	S	825	
ATT	GTT	TCC	TTA	TTG	TTA	ATC	CCT	TAT	CCA	TTG	TGT	TCC	2552
L	W	V	T	F	A	I	G	S	V	I	V	G	838
TTG	TGG	GTG	ACT	TTT	GCT	ATC	GGT	TCT	GTG	ATT	GTA	GGG	2591
V	T	G	F	M	A	F	W	K	V	N	L	D	851
GTA	ACG	GGT	TTC	ATG	GCA	TTC	TGG	AAA	GTC	AAT	CTT	GAT	2630

FIG. 3

11/18

S I S M I N L V I C T G F	864
TCC ATA TCC ATG ATT AAT CTT GTC ATT TGT ACA GGG TTT	2669
S F D F S A H I S Y A F V	877
TCT TTC GAT TTT TCT GCA CAC ATT TCC TAT GCA TTT GTT	2708
S S S Q P S V N Q K S V E	890
TCT AGT TCT CAA CCC TCA GTA AAC CAA AAA TCA GTT GAG	2747
A L Y L L G Y P V L Q S A	903
GCA TTG TAT CTT CTA GGC TAC CCA GTG TTA CAA AGT GCA	2786
I S T I I G V C V L A A A	916
ATT TCA ACA ATA ATA GGG GTG TGT GTT TTA GCT GCA GCG	2825
K A Y I F R T F F K I M F	929
AAA GCA TAC ATC TTC AGA ACA TTT TTT AAG ATT ATG TTT	2864
L V M I F G A A H G L I F	942
CTT GTT ATG ATA TTT GGG GCA GCT CAT GGC CTA ATT TTT	2903
I P V F L T F F G R F I *	955
ATT CCA GTA TTC TTA ACC TTT TTT GGA AGG TTT ATT TGA	2942
ATATCCACTAACAAAGTCAAAGACCAATTCTAGAATTCCCTGATTGCCCTATTC	2994
CAATCTGATTTTTAAATGCACTATTAAGAATAGTCACAAACTACTGGGA	3046
GGCAAAGTGGGTGGATCACCTGAGGTCAAGAATTGAGACCAGCCTGGCCA	3098
ACATGGTGAAACCTCGACACTACTGAAAATACAAAAATTATCCAGGCATGGT	3150
GGCGTGCACCTATAATCCCAGCTACCTGGGAGGCTGAGGCAGGAGAATCGCT	3202
TGAACCTGGGAGATGGAGGTTGCAGTGAGCTGGAGTGCACCAGGCACTCCAG	3254
CCTGGGTGACAAGAATGAGACTCCGTCTCAGAAAAAAAAAA	3296

FIG. 3

12/18

## HTPL-S

nt: SEQ ID NO: 4  
aa: SEQ ID NO: 6

CAGGAAACCGTCTGGTGGGATCTCCGCAGCTGCTTTCACCTGCTGTCCTC	52
M P W V E P	6
CTCCGCTTCCTAACAGAGGAAGAATCA ATG CCG TGG GTG GAG CCC	95
K P R P G P E Q K P K L T	19
AAG CCC AGG CCG GGG CCG GAG CAG AAG CCC AAG CTC ACC	134
K P D S A T G P Q W Y Q E	32
AAA CCG GAC TCT GCC ACC GGG CCG CAG TGG TAC CAG GAA	173
S Q E S E S E G K Q P P P	45
TCT CAG GAA TCG GAG TCG GAA GGC AAG CAG CCA CCC CCG	212
G P L A P P K S P E P S G	58
GGA CCC CTG GCA CCC CCG AAA TCC CCC GAA CCC TCA GGA	251
P L A S E Q D A P L P E G	71
CCC CTG GCG TCG GAG CAG GAT GCA CCC CTG CCA GAG GGG	290
D D A P P R P S M L D D A	84
GAC GAT GCA CCC CCC CGG CCG TCG ATG CTG GAC GAT GCA	329
P R L P L E L D D A P L P	97
CCC CGC CTG CCG CTG GAG CTG GAC GAT GCA CCC CTG CCG	368
E E E T P E P T A I C R H	110
GAG GAG GAA ACC CCC GAA CCC ACG GCC ATC TGC AGG CAC	407
R H R C H T D C L E G L L	123
CGG CAC CGC TGT CAC ACC GAC TGC CTA GAG GGG CTG CTG	446
S R T F Q W L G W Q V G A	136
TCC CGC ACC TTC CAG TGG CTG GGG TGG CAG GTG GGC GCG	485

FIG. 4

H	P	W	I	F	L	L	A	P	L	M	L	T		149
CAC	CCC	TGG	ATC	TTC	CTG	CTG	GCG	CCC	TTG	ATG	CTG	ACA		524
A	A	L	G	T	G	F	L	Y	L	P	K	D		162
GCC	GCG	CTG	GGC	ACC	GGC	TTC	CTG	TAC	CTA	CCC	AAG	GAC		563
E	E	E	D	L	E	E	H	Y	T	P	V	G		175
GAA	GAG	GAA	GAC	CTA	GAG	GAG	CAT	TAC	ACC	CCT	GTG	GGG		602
S	P	A	K	A	E	R	R	F	V	Q	G	H		188
AGC	CCG	GCC	AAG	GCG	GAG	CGG	CGC	TTC	GTG	CAG	GGC	CAT		641
F	T	T	N	D	S	Y	R	F	S	A	S	R		201
TTC	ACC	ACC	AAC	GAC	TCC	TAC	CGC	TTC	TCC	GCC	TCC	AGG		680
R	S	T	E	A	N	F	V	S	L	L	V	V		214
AGG	AGC	ACC	GAA	GCC	AAT	TTC	GTC	TCG	CTT	CTG	GTG	GTC		719
S	Y	S	D	S	L	L	D	P	A	T	F	A		227
TCC	TAC	AGC	GAC	TCA	CTG	CTG	GAC	CCA	GCT	ACC	TTT	GCA		758
E	V	S	K	L	D	G	A	V	Q	D	L	R		240
GAA	GTC	AGC	AAA	CTG	GAC	GGC	GCG	GTG	CAG	GAT	CTG	CGC		797
V	A	R	E	K	G	S	Q	I	Q	Y	Q	Q		253
GTG	GCG	CGG	GAA	AAG	GGA	AGC	CAG	ATC	CAG	TAC	CAG	CAG		836
V	C	A	R	Y	R	A	L	C	V	P	P	N		266
GTG	TGC	GCG	AGG	TAC	AGG	GGC	CTC	TGC	GTG	CCC	CCC	AAC		875
P	I	L	Y	A	W	Q	V	N	K	T	L	N		279
CCG	ATC	CTG	TAC	GCC	TGG	CAG	GTG	AAC	AAA	ACG	CTC	AAC		914
L	S	S	I	S	F	P	A	Y	N	H	G	R		292
CTG	AGC	AGC	ATC	TCC	TTC	CCC	GCC	TAC	AAC	CAC	GGC	AGG		953
H	P	L	Y	L	T	G	F	F	G	G	Y	I		305
CAT	CCC	CTC	TAC	CTG	ACC	GGC	TTC	TTC	GGA	GGA	TAC	ATC		992
L	G	G	S	L	G	M	G	Q	L	L	L	R		318
TTG	GGG	GGC	AGC	CTA	GGA	ATG	GGC	CAG	TTA	CTC	CTG	CGG		1031

FIG. 4

A	K	A	M	R	L	L	Y	Y	L	K	T	E	331
GCC	AAA	GCC	ATG	CGG	CTG	CTG	TAC	TAC	CTG	AAG	ACC	GAG	1070
D	P	E	Y	D	V	Q	S	K	Q	W	L	T	344
GAC	CCT	GAG	TAC	GAC	GTG	CAG	AGC	AAG	CAG	TGG	CTC	ACC	1109
H	L	L	D	Q	F	T	N	I	K	N	I	L	357
CAT	TTG	CTC	GAT	CAA	TTT	ACC	AAC	ATT	AAG	AAC	ATC	TTG	1148
A	L	K	K	I	E	V	V	H	F	T	S	L	370
GCC	TTG	AAA	AAA	ATT	GAG	GTA	GTC	CAC	TTT	ACA	TCG	CTT	1187
S	R	Q	L	E	F	E	A	T	S	V	T	V	383
TCC	AGA	CAA	CTG	GAA	TTT	GAG	GCA	ACT	TCT	GTG	ACT	GTG	1226
I	P	V	F	H	L	A	Y	I	L	I	I	L	396
ATC	CCT	GTG	TTT	CAC	CTG	GCA	TAC	ATT	CTC	ATC	ATT	CTG	1265
F	A	V	T	S	C	F	R	F	D	C	I	R	409
TTT	GCA	GTC	ACA	TCA	TGC	TTT	AGG	TTT	GAC	TGC	ATA	CGA	1304
N	K	M	C	V	A	A	F	G	V	I	S	A	422
AAC	AAA	ATG	TGT	GTT	GCG	GCC	TTT	GGA	GTG	ATT	TCT	GCT	1343
F	L	A	V	V	S	G	F	G	L	L	L	H	435
TTC	TTG	GCA	GTG	GTG	AGC	GGC	TTT	GGC	CTG	CTG	TTG	CAC	1382
I	G	V	P	F	V	I	I	V	A	N	S	P	448
ATT	GGG	GTG	CCA	TTT	GTC	ATC	ATA	GTT	GCC	AAT	TCA	CCA	1421
F	L	I	L	G	V	G	V	D	D	M	F	I	461
TTT	CTT	ATT	CTA	GGT	GTT	GGG	GTC	GAT	GAC	ATG	TTT	ATC	1460
M	I	S	A	W	H	K	T	N	L	A	D	D	474
ATG	ATT	TCT	GCC	TGG	CAT	AAG	ACC	AAC	CTT	GCA	GAT	GAC	1499
I	R	E	R	M	S	N	V	Y	S	K	A	A	487
ATA	CGA	GAG	CGG	ATG	TCC	AAT	GTC	TAT	TCA	AAA	GCG	GCA	1538
V	S	I	T	I	T	T	I	T	N	I	L	A	500
GTG	TCT	ATT	ACA	ATC	ACC	ACC	ATC	ACT	AAC	ATC	CTG	GCC	1577

FIG. 4

15/18

L	Y	T	G	I	M	S	S	F	R	S	V	Q		513
TTA	TAT	ACA	GGG	ATT	ATG	AGC	TCT	TTT	AGG	TCT	GTA	CAA		1616
C	F	C	I	Y	T	G	M	T	L	L	F	C		526
TGT	TTT	TGC	ATC	TAT	ACA	GGA	ATG	ACC	CTG	TTA	TTT	TGC		1655
Y	F	Y	N	I	T	C	F	G	A	F	M	A		539
TAT	TTT	TAT	AAC	ATC	ACG	TGT	TTT	GGA	GCA	TTT	ATG	GCC		1694
L	D	G	K	R	E	V	V	C	L	C	W	L		552
TTG	GAT	GGT	AAA	AGA	GAA	GTA	GTC	TGC	CTA	TGC	TGG	TTG		1733
K	K	A	D	P	K	W	P	S	F	K	K	F		565
AAA	AAG	GCT	GAC	CCA	AAA	TGG	CCC	TCA	TTT	AAA	AAG	TTC		1772
C	C	F	P	F	G	S	V	P	D	E	H	G		578
TGC	TGT	TTC	CCA	TTT	GGT	TCT	GTC	CCA	GAT	GAA	CAT	GGA		1811
T	D	I	H	P	I	S	L	F	F	R	D	Y		591
ACT	GAT	ATC	CAT	CCA	ATA	AGT	TTG	TTT	TTT	AGA	GAC	TAT		1850
F	G	P	F	L	T	R	S	E	S	K	Y	F		604
TTT	GGC	CCC	TTT	CTC	ACA	AGG	AGT	GAG	TCC	AAG	TAT	TTT		1889
V	V	F	I	Y	V	L	Y	I	I	S	S	I		617
GTA	GTC	TTT	ATA	TAT	GTG	TTG	TAC	ATC	ATA	AGC	AGT	ATA		1928
Y	G	C	F	H	V	Q	E	G	L	D	L	R		630
TAT	GGG	TGT	TTC	CAT	GTG	CAG	GAA	GGT	TTA	GAC	CTT	CGA		1967
N	L	A	S	D	D	S	Y	I	T	P	Y	F		643
AAT	CTG	GCA	AGT	GAC	GAT	TCC	TAC	ATC	ACA	CCA	TAT	TTT		2006
N	V	E	E	N	Y	F	S	D	Y	G	P	R		656
AAC	GTA	GAG	GAG	AAT	TAT	TTT	TCA	GAT	TAT	GGT	CCC	AGG		2045
V	M	V	I	V	T	K	K	V	D	Y	W	D		669
GTT	ATG	GTT	ATT	GTT	ACT	AAA	AAA	GTT	GAC	TAC	TGG	GAT		2084
K	D	V	R	Q	K	L	E	N	C	T	K	I		682
AAA	GAT	GTT	AGG	CAA	AAA	CTG	GAA	AAC	TGT	ACT	AAA	ATT		2123
F	E	K	N	V	Y	V	D	K	N	L	T	E		695
TTT	GAA	AAA	AAT	GTC	TAT	GTA	GAT	AAA	AAT	CTT	ACA	GAG		2162

FIG. 4

16/18

F	W	L	D	A	Y	V	Q	Y	L	K	G	N	708
TTT	TGG	TTA	GAT	GCA	TAT	GTG	CAA	TAT	TTA	AAA	GGT	AAC	2201
S	Q	D	P	N	E	K	N	T	F	M	N	N	721
AGC	CAA	GAT	CCT	AAT	GAG	AAG	AAT	ACT	TTT	ATG	AAC	AAT	2240
I	P	D	F	L	S	N	F	P	N	F	Q	H	734
ATT	CCT	GAT	TTT	TTA	AGC	AAT	TTT	CCA	AAT	TTT	CAG	CAT	2279
D	I	N	I	S	S	S	N	E	I	I	S	S	747
GAT	ATT	AAT	ATT	TCT	TCA	TCA	AAT	GAA	ATC	ATT	TCT	TCC	2318
R	G	F	I	Q	T	T	D	V	S	S	S	A	760
CGG	GGC	TTC	ATT	CAG	ACA	ACA	GAT	GTT	TCT	TCC	TCA	GCC	2357
K	K	K	I	L	L	F	*						768
AAA	AAG	AAA	ATA	TTG	TTA	TTC	TAA						2400
ACTGTC	AAATTCCC	CTAATGGT	GATAACCAGGC	ATTTAT	ATATTG	ATCA							2452
GTATGCTG	CAATATTAGA	AGACACTG	TTAGAA	ATGTATTG	GTTCAT	CAGCA							2504
GCTATGTT	CATTGTT	CCCTATTGTT	TAATCC	TTATCC	ATTGTG	TTGCCTTGT							2556
GGGTGACT	TTTGCTATTGGT	TCTGTGATTG	TAGGGTAACGGG	TTTCATGGC									2608
ATTCTGGAA	AGTC	ATCTGATTCC	CATATCC	ATGATT	AAATCTTGT	CATTG							2660
ATAGGG	TTTCTTC	GATTTCTGT	ACACATT	TCCTATGC	ATTGTT	CTA							2712
GTTCTCA	ACCCTCAGT	AAACCAAA	ATCAGTTGAGGC	ATTGT	TATCTT	CTAGG							2764
CTACCCAGT	GTTACAAAG	TGCAATT	CAACAATA	ATAGGGT	GTGTG	TTTA							2816
GCTGCAGCG	AAAGCATAC	ATCTTCAGAAC	ATT	TTTAAG	ATTATG	TTCTTG							2868
TTATGAT	ATTGGGGCAG	CTCATGGC	CTAATT	TTTATTCC	AGTATT	CTTAAC							2920
CTTTTTGG	AAAGGTT	TATTGA	ATATCC	ACTAACAA	AGTC	AAAGACCA	ATTCT						2972
AGAATT	CCTGATTGCC	CTATTCCA	ATCTG	ATT	TTTAA	ATGC	ACTATT	AAG					3024
AATAGTC	ACAAACTACT	GGGAGGCC	AAAGGT	GGGTGG	ATCAC	CTGAGGT	CAA						3076

**FIG. 4**

17/18

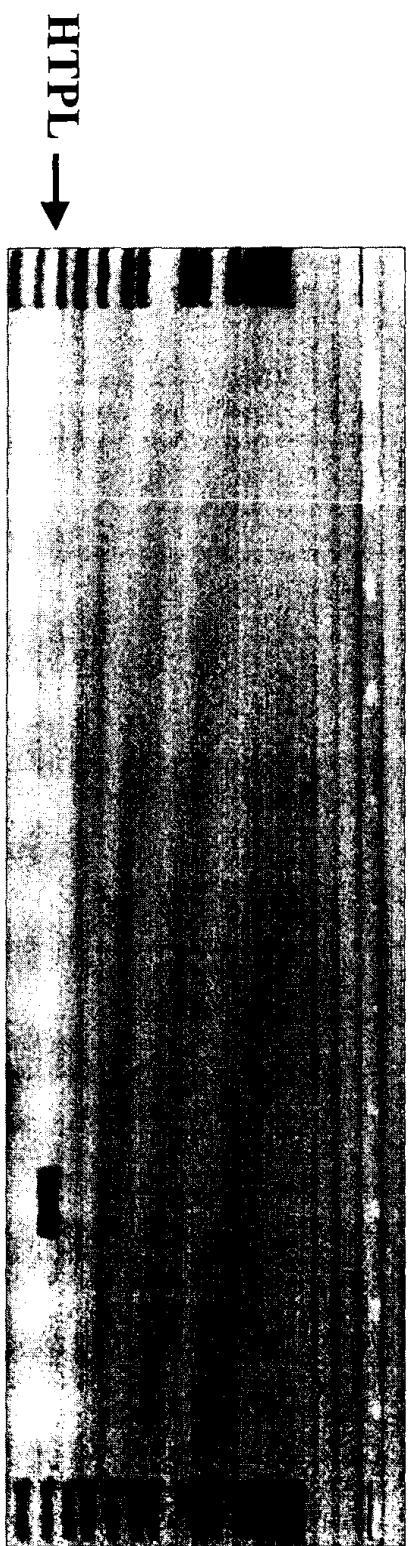
GAATTCGAGACCAGCCTGGCCAACATGGTGAACCTCGACACTACTGAAAAT	3128
ACAAAAAATTATCCAGGCATGGTGGCGTGCACCTATAATCCCAGCTACCTGGG	3180
AGGCTGAGGCAGGAGAACATCGCTTGAACCTGGGAGATGGAGGTTGCAGTGAGC	3232
TGGAGTGCACCAGGCACTCCAGCCTGGGTGACAAGAATGAGACTCCGTCTCA	3284
GAAAAAAAAAAAAAA	3298

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

**FIG. 4**

## **HTPL tissue distribution by RT-PCR**

**brain**  
**heart**  
**skeletal muscle**  
**bone marrow**  
**lung**  
**liver**  
**kidney**  
**colon**  
**testis**  
**placenta**  
**uterus**  
**marker**



**FIG. 5**